W736: Facing the Challenges of Coconut Genetic Improvement: The Coconut Genome

Sunday, January 14, 2018
04:30 PM - 05:00 PM
Towne - Meeting House

Coconut is an integral part of the livelihood of millions of farmers in the coastal tropical areas and is facing an important mutation. While its place as a major cheap oil crop on the international market is slowly declining, promising markets are emerging, such as coconut water, virgin coconut oil, and sugar among others. Coconut is regaining its tradition role of multi-usage crop, leading to new opportunities. It is however facing serious threats such as widespread lethal diseases and insect pests. To meet these challenges, coconut genetic improvement should renew its practices and objectives. But it is a difficult task due to long generation duration, low planting densities and low prolificacy. Advances in coconut genomic studies will improve its efficiency in several ways: Neutral markers allow broadening the genetic base of selection; QTLs based on mapping populations or on whole genome association studies (GWAS) will reduce the time and the areas needed to establish a breeding program. Comparative genomics and transcriptomics provide an in-depth understanding of metabolic pathways involved in production, product quality and adaptation to biotic and abiotic stress. A coconut genome draft was published recently and will be converted into a reference sequence thanks to high-density linkage mapping. Other sequencing efforts have been undertaken, whose combined results will provide a preliminary basis for characterizing coconut genetic diversity at the gene level to be completed by more resequencing. A revival of coconut genetic improvement will depend, among other elements, on high quality phenotyping, in conjunction with large SNP sets, transcriptomics and comparative genomics.

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